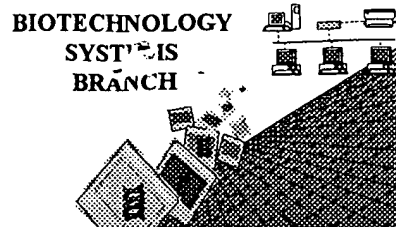# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

RECEIVED

Application Serial Number: _09/757,655_

Source: _/600_

Date Processed by STIC: _2/21/2002_

MAR 0 8 2002

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE**
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A**
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission
   User Manual - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:
For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support (SIRA)
      Technical Assistance...703-287-0200
      To Purchase PatentIn Software.......................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

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MAR 0 8 2002

TECH CENTER 1600/2900

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002
TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt
Output Set: N:\CRF3\02212002\I757655.raw

Does Not Comply
Corrected Diskette Needed

pp 1-5

```
 3 <110> APPLICANT: FUJII, Takeru
 4         YOKOYAMA, Hideakira
 5         HAMAMOTO, Hidetoshi
 7 <120> TITLE OF INVENTION: A PEPTIDE HAVING AN AFFINITY FOR gp120
 9 <130> FILE REFERENCE: 2001-0019A/LC/01732
11 <140> CURRENT APPLICATION NUMBER: 09/757,655
12 <141> CURRENT FILING DATE: 2001-01-11
14 <150> PRIOR APPLICATION NUMBER: JP No. 2000-6182
15 <151> PRIOR FILING DATE: 2000-01-11
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 5
23 <212> TYPE: PRT
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
29 <220> FEATURE:
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insufficient Explanation - give source of genetic material (see item 11 on Error Summary Sheet)

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W--> 30 <221> NAME/KEY: Residue
     31 <222> LOCATION: (1)
     32 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr
     34 <220> FEATURE:
W--> 35 <221> NAME/KEY: Residue
     36 <222> LOCATION: (2)
     37 <223> OTHER INFORMATION: Xaa = Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr
     39 <220> FEATURE:
W--> 40 <221> NAME/KEY: Residue
     41 <222> LOCATION: (3)
     42 <223> OTHER INFORMATION: Xaa = Lys, Val, Asp, Arg, Ala or Trp
     44 <220> FEATURE:
W--> 45 <221> NAME/KEY: Residue
     46 <222> LOCATION: (4)
     47 <223> OTHER INFORMATION: Xaa = Ala, Trp or Gly
     49 <220> FEATURE:
W--> 50 <221> NAME/KEY: Residue
     51 <222> LOCATION: (5)
     52 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
     53         Phe, Trp, Pro or Tyr
     55 <400> SEQUENCE: 1
     56 Xaa Xaa Xaa Xaa Xaa
     57  1               5
     59 <210> SEQ ID NO: 2
     60 <211> LENGTH: 5
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RAW SEQUENCE LISTING   DATE: 02/21/2002
PATENT APPLICATION: US/09/757,655   TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt
Output Set: N:\CRF3\02212002\I757655.raw

```
        61 <212> TYPE: PRT
        62 <213> ORGANISM: Artificial Sequence
        64 <220> FEATURE:
        65 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
        67 <220> FEATURE:
W--> 68 <221> NAME/KEY: Residue
        69 <222> LOCATION: (1)
        70 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr, or polypeptide
residue that an
        71        arbitrary amino acid stood in line in the N-terminal side from this amino acid
        73 <220> FEATURE:
W--> 74 <221> NAME/KEY: Residue
        75 <222> LOCATION: (2)
        76 <223> OTHER INFORMATION: Xaa = Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr
        78 <220> FEATURE:
W--> 79 <221> NAME/KEY: Residue
        80 <222> LOCATION: (3)
        81 <223> OTHER INFORMATION: Xaa = Lys, Val, Asp, Arg, Ala or Trp
        83 <220> FEATURE:
W--> 84 <221> NAME/KEY: Residue
        85 <222> LOCATION: (4)
        86 <223> OTHER INFORMATION: Xaa = Ala, Trp or Gly
        88 <220> FEATURE:
W--> 89 <221> NAME/KEY: Residue
        90 <222> LOCATION: (5)
        91 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
        92        Phe, Trp, Pro or Tyr
        94 <400> SEQUENCE: 2
W--> 95 Xaa Xaa Xaa Xaa Xaa
        96  1                5
        98 <210> SEQ ID NO: 3
        99 <211> LENGTH: 5
       100 <212> TYPE: PRT
       101 <213> ORGANISM: Artificial Sequence
       103 <220> FEATURE:
       104 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
       106 <220> FEATURE:
W--> 107 <221> NAME/KEY: Residue
       108 <222> LOCATION: (1)
       109 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr
       111 <220> FEATURE:
W--> 112 <221> NAME/KEY: Residue
       113 <222> LOCATION: (2)
       114 <223> OTHER INFORMATION: Xaa = Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr
       116 <220> FEATURE:
W--> 117 <221> NAME/KEY: Residue
       118 <222> LOCATION: (3)
       119 <223> OTHER INFORMATION: Xaa = Lys, Val, Asp, Arg, Ala or Trp
       121 <220> FEATURE:
W--> 122 <221> NAME/KEY: Residue
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002
TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt
Output Set: N:\CRF3\02212002\I757655.raw

```
        123 <222> LOCATION: (4)
        124 <223> OTHER INFORMATION: Xaa = Ala, Trp or Gly
        126 <220> FEATURE:
W-->    127 <221> NAME/KEY: Residue
        128 <222> LOCATION: (5)
        129 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Thr, Met, Asn, Gln, His, Lys,
Arg,
        130         Phe, Trp, Pro or Tyr, or polypeptide residue that an arbitrary amino acid
        131         stood in line in the C-terminal side of this amino acid, H
        133 <400> SEQUENCE: 3
        134 Xaa Xaa Xaa Xaa Xaa
        135   1               5
        138 <210> SEQ ID NO: 4
        139 <211> LENGTH: 5
        140 <212> TYPE: PRT
        141 <213> ORGANISM: Artificial Sequence
        143 <220> FEATURE:
        144 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
        146 <220> FEATURE:
W-->    147 <221> NAME/KEY: Residue
        148 <222> LOCATION: (1)
        149 <223> OTHER INFORMATION: Xaa = Tyr, Arg, Phe, Gly, Trp, His or Asp
        151 <220> FEATURE:
W-->    152 <221> NAME/KEY: Residue
        153 <222> LOCATION: (2)
        154 <223> OTHER INFORMATION: Xaa = Arg, Tyr, Trp, Ala, Val, Gln, His or Lys
        156 <220> FEATURE:
W-->    157 <221> NAME/KEY: Residue
        158 <222> LOCATION: (3)
        159 <223> OTHER INFORMATION: Xaa = Lys, Tyr, Arg, Glu, Met or Trp
        161 <220> FEATURE:
W-->    162 <221> NAME/KEY: Residue
        163 <222> LOCATION: (4)
        164 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
        165         Phe or Trp
        167 <220> FEATURE:
W-->    168 <221> NAME/KEY: Residue
        169 <222> LOCATION: (5)
        170 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
        171         Phe, Tyr or Trp
        173 <400> SEQUENCE: 4
        174 Xaa Xaa Xaa Xaa Xaa
        175   1               5
        177 <210> SEQ ID NO: 5
        178 <211> LENGTH: 5
        179 <212> TYPE: PRT
        180 <213> ORGANISM: Artificial Sequence
        182 <220> FEATURE:
        183 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
        185 <220> FEATURE:
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002
TIME: 11:38:41

Input Set : **A:\FUJII SEQUENCE LISTING.txt**
Output Set: **N:\CRF3\02212002\I757655.raw**

```
W--> 186 <221> NAME/KEY: Residue
     187 <222> LOCATION: (1)
     188 <223> OTHER INFORMATION: Xaa = Tyr, Arg, Phe, Gly, Trp, His or Asp, or polypeptide
residue that an
     189       arbitrary amino acid stood in the N-terminal side from this amino acid
     191 <220> FEATURE:
W--> 192 <221> NAME/KEY: Residue
     193 <222> LOCATION: (2)
     194 <223> OTHER INFORMATION: Xaa = Arg, Tyr, Trp, Ala, Val, Gln, His or Lys
     196 <220> FEATURE:
W--> 197 <221> NAME/KEY: Residue
     198 <222> LOCATION: (3)
     199 <223> OTHER INFORMATION: Xaa = Lys, Tyr, Arg, Glu, Met or Trp
     201 <220> FEATURE:
W--> 202 <221> NAME/KEY: Residue
     203 <222> LOCATION: (4)
     204 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
     205       Phe or Trp
     207 <220> FEATURE:
W--> 208 <221> NAME/KEY: Residue
     209 <222> LOCATION: (5)
     210 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
     211       Phe, Tyr or Trp
     213 <400> SEQUENCE: 5
     214 Xaa Xaa Xaa Xaa Xaa
     215  1                 5
     217 <210> SEQ ID NO: 6
     218 <211> LENGTH: 5
     219 <212> TYPE: PRT
     220 <213> ORGANISM: Artificial Sequence
     222 <220> FEATURE:
     223 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
     225 <220> FEATURE:
W--> 226 <221> NAME/KEY: Residue
     227 <222> LOCATION: (1)
     228 <223> OTHER INFORMATION: Xaa = Tyr, Arg, Phe, Gly, Trp, His or Asp
     230 <220> FEATURE:
W--> 231 <221> NAME/KEY: Residue
     232 <222> LOCATION: (2)
     233 <223> OTHER INFORMATION: Xaa = Arg, Tyr, Trp, Ala, Val, Gln, His or Lys
     235 <220> FEATURE:
W--> 236 <221> NAME/KEY: Residue
     237 <222> LOCATION: (3)
     238 <223> OTHER INFORMATION: Xaa = Lys, Tyr, Arg, Glu, Met or Trp
     240 <220> FEATURE:
W--> 241 <221> NAME/KEY: Residue
     242 <222> LOCATION: (4)
     243 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
     244       Phe or Trp
     246 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 02/21/2002
PATENT APPLICATION: US/09/757,655 TIME: 11:38:41

Input Set : **A:\FUJII SEQUENCE LISTING.txt**
Output Set: **N:\CRF3\02212002\I757655.raw**

```
W--> 247 <221> NAME/KEY: Residue
     248 <222> LOCATION: (5)
     249 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
     250        Phe, Tyr or Trp, or polypeptide residue that an arbitrary amino acid stood in
line
     251        in the C-terminal side of this amino acid
     253 <400> SEQUENCE: 6
W--> 254 Xaa Xaa Xaa Xaa Xaa
     255   1               5
     257 <210> SEQ ID NO: 7
     258 <211> LENGTH: 7
     259 <212> TYPE: PRT
     260 <213> ORGANISM: Artificial Sequence
     262 <220> FEATURE:
     263 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
     265 <400> SEQUENCE: 7
     266 Gly Gly Asp Val Lys Ala Gly
     267   1               5
     269 <210> SEQ ID NO: 8
     270 <211> LENGTH: 6
     271 <212> TYPE: PRT
     272 <213> ORGANISM: Artificial Sequence
     274 <220> FEATURE:
     275 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
     277 <400> SEQUENCE: 8
     278 Gly Asp Val Lys Ala Gly
     279   1               5
     281 <210> SEQ ID NO: 9
     282 <211> LENGTH: 6
     283 <212> TYPE: PRT
     284 <213> ORGANISM: Artificial Sequence
     286 <220> FEATURE:
     287 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
     289 <400> SEQUENCE: 9
     290 Gly Tyr Tyr Lys Ala Ala
     291   1               5
     293 <210> SEQ ID NO: 10
     294 <211> LENGTH: 6
     295 <212> TYPE: PRT
     296 <213> ORGANISM: Artificial Sequence
     298 <220> FEATURE:
     299 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
     301 <400> SEQUENCE: 10
     302 Gly Tyr Ala Tyr Arg Lys
     303   1               5
     305 <210> SEQ ID NO: 11
     306 <211> LENGTH: 6
     307 <212> TYPE: PRT
     308 <213> ORGANISM: Artificial Sequence
     310 <220> FEATURE:
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Please correct this error in subsequent sequences

VERIFICATION SUMMARY   DATE: 02/21/2002
PATENT APPLICATION: **US/09/757,655**   TIME: 11:38:42

Input Set : **A:\FUJII SEQUENCE LISTING.txt**
Output Set: **N:\CRF3\02212002\I757655.raw**

```
L:30 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:35 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:40 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:45 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:50 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:68 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:74 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:79 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:84 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:89 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:107 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:112 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:117 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:122 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:127 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:147 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:152 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:157 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:162 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:168 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:186 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:197 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:202 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:208 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:226 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:231 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:236 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:241 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:247 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
```

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/757,655_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
(OLD RULES)

Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001